Claims

1. An isolated nucleic acid molecule selected from the group consisting of:

(a) nucleic acid molecules which hybridize under stringent conditions to a molecule consisting of a nucleotide sequence set forth as SEQ ID NO:1 and which code for a human *vasa* polypeptide,

(b) nucleic acid molecules that differ from the nucleic acid molecules of (a) or (b) in codon sequence due to the degeneracy of the genetic code, or

(c) complements of (a) or (b).

2. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule comprises the nucleotide sequence set forth as SEQ ID NO:1.

3. The isolated nucleic acid molecule of claim 1, wherein the isolated nucleic acid molecule consists of the nucleotide sequence set forth as SEQ ID NO:15 or a fragment thereof.

4. An isolated nucleic acid molecule selected from the group consisting of

(a) unique fragments of a nucleotide sequence set forth as SEQ ID NO:1,

(b) complements of (a),

provided that a unique fragment of (a) includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the sequence group consisting of

(1) sequences having the database accession numbers of Table I, or sequences encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7,

(2) complements of (1), and

(3) fragments of (1) and (2).

5. The isolated nucleic acid molecule of claim 4, wherein the sequence of contiguous nucleotides is selected from the group consisting of:

(1) at least two contiguous nucleotides nonidentical to the sequence group,

(2) at least three contiguous nucleotides nonidentical to the sequence group,

(3) at least four contiguous nucleotides nonidentical to the sequence group,

(4) at least five contiguous nucleotides nonidentical to the sequence group,

(5) at least six contiguous nucleotides nonidentical to the sequence group,

(6) at least seven contiguous nucleotides nonidentical to the sequence group.

6. The isolated nucleic acid molecule of claim 4, wherein the fragment has a size selected from the group consisting of at least: 8 nucleotides, 10 nucleotides, 12 nucleotides, 14 nucleotides, 16 nucleotides, 18 nucleotides, 20, nucleotides, 22 nucleotides, 24 nucleotides, 26 nucleotides, 28 nucleotides, 30 nucleotides, 50 nucleotides, 75 nucleotides, 100 nucleotides, and 200 nucleotides.

7. The isolated nucleic acid molecule of claim 4, wherein the molecule encodes a polypeptide which is immunogenic.

8. An expression vector comprising the isolated nucleic acid molecule of claims 1, 2, 3, 4, 5, 6, or 7 operably linked to a promoter.

9. An expression vector comprising the isolated nucleic acid molecule of claim 4 operably linked to a promoter.

10. A host cell transformed or transfected with the expression vector of claim 8.

11. A host cell transformed or transfected with the expression vector of claim 9.

12. An isolated polypeptide encoded by the isolated nucleic acid molecule of claim 1, ~~2, 3, or 4~~, wherein the polypeptide, or fragment of the polypeptide, has germ cell specific expression.

13. The isolated polypeptide of claim 12, wherein the isolated polypeptide is encoded by the isolated nucleic acid molecule of claim 2.

14. The isolated polypeptide of claim 13, wherein the isolated polypeptide comprises a polypeptide having the sequence of amino acids 1-724 of SEQ ID NO:2.

15. An isolated polypeptide encoded by the isolated nucleic acid molecule of claim 1, 2, 3, or 4, wherein the polypeptide, or fragment of the polypeptide, is immunogenic.

16. The fragment of claim 15, wherein the fragment, or portion of the fragment, binds to a human antibody.

17. An isolated binding polypeptide which binds selectively a polypeptide encoded by the isolated nucleic acid molecule of claim 1, ~~2, 3 or 4~~.

18. The isolated binding polypeptide of claim 17, wherein the isolated binding polypeptide binds to a polypeptide having the sequence of amino acids of SEQ ID NO:2.

19. The isolated binding polypeptide of claim 17, wherein the isolated binding polypeptide binds to a polypeptide having the sequence of amino acids of SEQ ID NO:9 or SEQ ID NO:10.

20. The isolated binding polypeptide of any one of claims 18 or 19, wherein the isolated binding polypeptide is an antibody or an antibody fragment selected from the group consisting of a Fab fragment, a $F(ab)_2$ fragment or a fragment including a CDR3 region selective for the polypeptide having the sequence of amino acids selected from the group consisting of SEQ ID NO:2, SEQ ID NO:9, and SEQ ID NO:10.

21. An isolated polypeptide comprising a fragment of the polypeptide of claim 12 having germ cell specific expression, provided that the fragment excludes a sequence of contiguous amino acids selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, and SEQ ID NO:7, or is encoded by an isolated nucleic acid having a nucleotide sequence with a GenBank database accession number as described in Table I.

22. A kit, comprising a package containing:

an agent that selectively binds to the isolated nucleic acid of claim 1 or an expression product thereof, and

a control for comparing to a measured value of binding of said agent to said isolated nucleic acid of claim 1 or expression product thereof.

23. The kit of claim 22, wherein the control is a predetermined value for comparing to the measured value.

24. The kit of claim 23, wherein the control comprises an epitope of the expression product of the nucleic acid of claim 1.

25. A method for determining the level of a *vasa* molecule expression in a subject, comprising:

a) obtaining a test sample from a subject,

b) measuring the expression of a *vasa* molecule in the test sample,

c) comparing the measured expression of the *vasa* molecule to a control.

26. The method of claim 25, wherein the expression of a *vasa* molecule in (b) is *vasa* mRNA expression.

27. The method of claim 25, wherein the expression of a *vasa* molecule in (b) is *vasa* polypeptide expression.

28. The method of claim 25, wherein the test sample is tissue.

29. The method of claim 25, wherein the test sample is a biological fluid.

30. The method of claim 25, wherein the test sample is a fine needle aspirate.

31. The method of claim 26, wherein *vasa* mRNA expression is measured using the Polymerase Chain Reaction (PCR).

32. The method of claim 26, wherein *vasa* mRNA expression is measured using northern blotting.

33. The method of claim 27, wherein *vasa* polypeptide expression is measured using a monoclonal antibody to a *vasa* polypeptide.

34. The method of claim 27, wherein *vasa* polypeptide expression is measured using polyclonal antisera to a *vasa* polypeptide.

35. A method of detecting a tumor of germ cell origin in an extragonadal sample, the method comprising:

detecting *vasa* expression in an extragonadal test sample obtained from a subject, wherein *vasa* expression in the extragonadal test sample is indicative of a tumor of germ cell origin in the subject.

36. The method of claim 35, wherein *vasa* expression is *vasa* mRNA expression.

37. The method of claim 35, wherein *vasa* expression is *vasa* polypeptide expression.

38. The method of claim 35, wherein the extragonadal test sample is tissue.

39. The method of claim 35, wherein the extragonadal test sample is a biological fluid.

40. The method of claim 35, wherein the test sample is a fine needle aspirate.

41. The method of claim 36, wherein *vasa* mRNA expression is measured using the Polymerase Chain Reaction.

42. The method of claim 36, wherein *vasa* mRNA expression is measured using northern blotting.

43. The method of claim 37, wherein *vasa* polypeptide expression is measured using a monoclonal antibody to a *vasa* polypeptide.

44. The method of claim 37, wherein *vasa* polypeptide expression is measured using polyclonal antisera to a *vasa* polypeptide.

45. The method of claim 35, wherein the subject has not previously been diagnosed as having a tumor of germ cell origin or a predisposition thereto.

46. The method of claim 35, wherein the subject has a clinical diagnosis of a tumor of germ cell origin and the method is to confirm the clinical diagnosis, monitor a remission of the tumor, or stage the tumor.

47. A method of detecting a tumor of germ cell origin, the method comprising:

detecting *vasa* overexpression in a test sample obtained from a subject, wherein *vasa* overexpression in the test sample as compared to a control is indicative of a tumor of germ cell origin in the subject.

48. The method of claim 47, wherein *vasa* overexpression is *vasa* mRNA overexpression.

49. The method of claim 47, wherein *vasa* overexpression is *vasa* polypeptide overexpression.

50. The method of claim 47, wherein the test sample is tissue.

51. The method of claim 47, wherein the test sample is a biological fluid.

52. The method of claim 47, wherein the test sample is a fine needle aspirate.

53. The method of claim 48, wherein *vasa* mRNA overexpression is measured using the Polymerase Chain Reaction (PCR).

54. The method of claim 48, wherein *vasa* mRNA overexpression is measured using northern blotting.

55. The method of claim 49, wherein *vasa* polypeptide overexpression is measured using a monoclonal antibody to a *vasa* polypeptide.

56. The method of claim 49, wherein *vasa* polypeptide overexpression is measured using polyclonal antisera to a *vasa* polypeptide.

57. The method of claim 47, wherein the tumor is selected from the group consisting of a testicular tumor, an ovarian tumor, and a tumor of an extragonadal tissue.

58. The method of claim 47, wherein the tumor is a testicular tumor.

59. The method of claim 47, wherein the tumor is an ovarian tumor.

60. The method of claim 47, wherein the tumor is a tumor of an extragonadal tissue.

61. The method of claim 47, wherein the tumor is a seminoma.

62. The method of claim 47, further comprising detecting expression of a tumor-specific agent other than a *vasa* molecule in the test sample.

63. The method of claim 62, wherein the tumor-specific agent other than a *vasa* molecule is selected from the group consisting of β-hCG, α-fetoprotein, placental-type alkaline phosphatase, prostate specific antigen, carcinoembryonic antigen, inhibin, epithelial membrane antigen, desmin, vimentin, GFAP, synaptophysin, chromogranin, cytokeratin isoforms, and anti-keratin markers.

64. The method of claim 47, wherein the subject has not previously been diagnosed as having a tumor of germ cell origin or a predisposition thereto.

65. The method of claim 47, wherein the subject has a clinical diagnosis of a tumor of germ cell origin and the method is to confirm the clinical diagnosis, monitor a remission of the tumor, or stage the tumor.

66. A method of subtyping tumors of germ cell origin, comprising:

detecting *vasa* expression in a test sample of a known or suspected tumor of germ cell origin obtained from a subject, wherein *vasa* overexpression in the test sample as compared to a control is indicative of a seminoma in the subject, or wherein absence of *vasa* expression in the test sample as compared to a control is indicative of a nonseminoma in the subject.

67. The method of claim 66, wherein *vasa* expression is *vasa* mRNA expression.

68. The method of claim 66, wherein *vasa* expression is *vasa* polypeptide expression.

69. The method of claim 66, wherein the test sample is tissue.

70. The method of claim 66, wherein the test sample is a biological fluid.

71. The method of claim 66, wherein the test sample is a fine needle aspirate.

72. The method of claim 67, wherein *vasa* mRNA expression is measured using the Polymerase Chain Reaction (PCR).

73. The method of claim 67, wherein *vasa* mRNA expression is measured using northern blotting.

74. The method of claim 68, wherein *vasa* polypeptide expression is measured using a monoclonal antibody to a *vasa* polypeptide.

75. The method of claim 68, wherein *vasa* polypeptide expression is measured using polyclonal antisera to a *vasa* polypeptide.

76. The method of claim 66, wherein the tumor is selected from the group consisting of a testicular tumor, an ovarian tumor, and a tumor of an extragonadal tissue.

77. The method of claim 66, wherein the tumor is a testicular tumor.

78. The method of claim 66, wherein the tumor is an ovarian tumor.

79. The method of claim 66, wherein the tumor is a tumor of an extragonadal tissue.

80. The method of claim 66, wherein the nonseminoma is selected from the group consisting of an embryonal carcinoma, a teratoma, a choriocarcinoma, a yolk sac tumor, or combinations of the foregoing.

81. The method of claim 66, wherein the subject has not previously been diagnosed as having a tumor of germ cell origin or a predisposition thereto.

82. The method of claim 66, wherein the subject has a clinical diagnosis of a tumor of germ cell origin and the method is to confirm the clinical diagnosis, monitor a remission of the tumor, or stage the tumor.

83. The method of claim 66, wherein the subject has a clinical diagnosis of a tumor of mixed histologic appearance.

84. The method of claim 66, further comprising detecting expression of a tumor-specific agent other than a *vasa* molecule in the test sample.

85. The method of claim 84, wherein the tumor-specific agent other than a *vasa* molecule is selected from the group consisting of β-hCG, α-fetoprotein, placental-type alkaline phosphatase, prostate specific antigen, carcinoembryonic antigen, inhibin, epithelial membrane antigen, desmin, vimentin, GFAP, synaptophysin, chromogranin, cytokeratin isoforms, and anti-keratin markers.

86. A method of distinguishing a tumor of germ cell origin from a non-germ cell tumor, the method comprising:

detecting expression of a *vasa* molecule in a test sample, wherein expression of the *vasa* molecule is indicative of a tumor of a germ cell origin and absence of expression of the *vasa* molecule is indicative of a non-germ cell tumor.

87. The method of claim 86, wherein the non-germ cell tumor resembles histologically a tumor of germ cell origin.

88. The method of claim 86, wherein the non-germ cell tumor is selected from the group consisting of a clear cell carcinoma of the ovary, a mediastinal thymoma, and a testicular lymphoma.